

1/52

#7

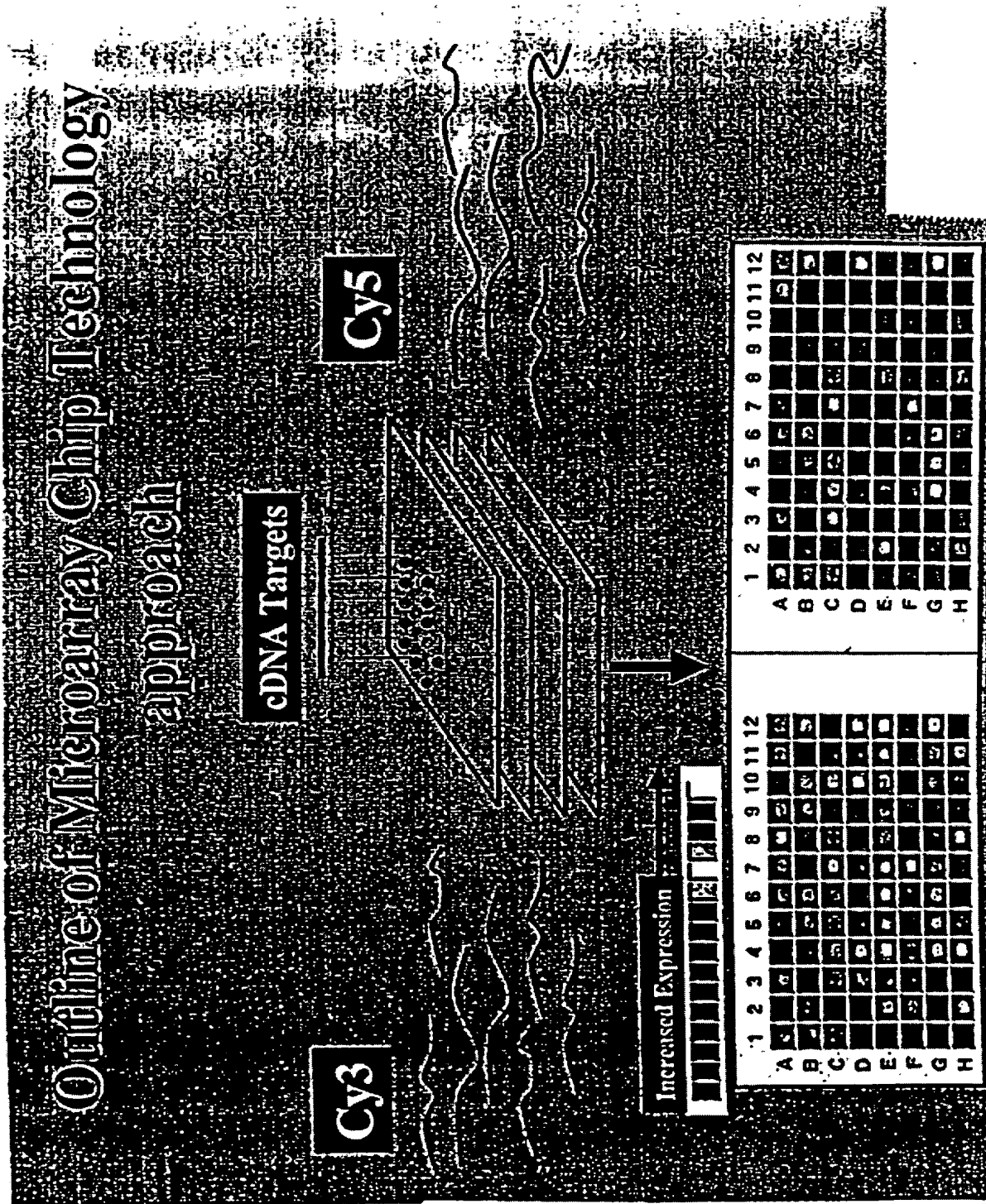
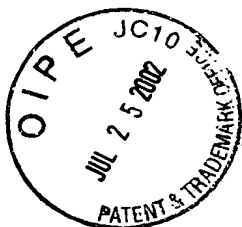


FIG. 1





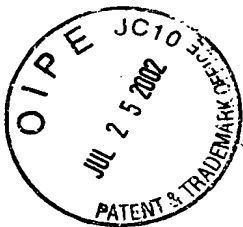
**LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS**

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins <small>see RNA 959</small>	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell <small>see RNA 958</small>	CL155	SPACT73	Heart N
Lymphoma, B cell	844	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.  
 RED: Normal essential tissue probes where gene expression is to be avoided.  
 BLACK : Normal tissue probes where gene expression is acceptable.



**FIG. 5**



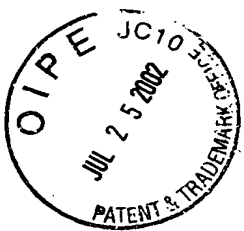
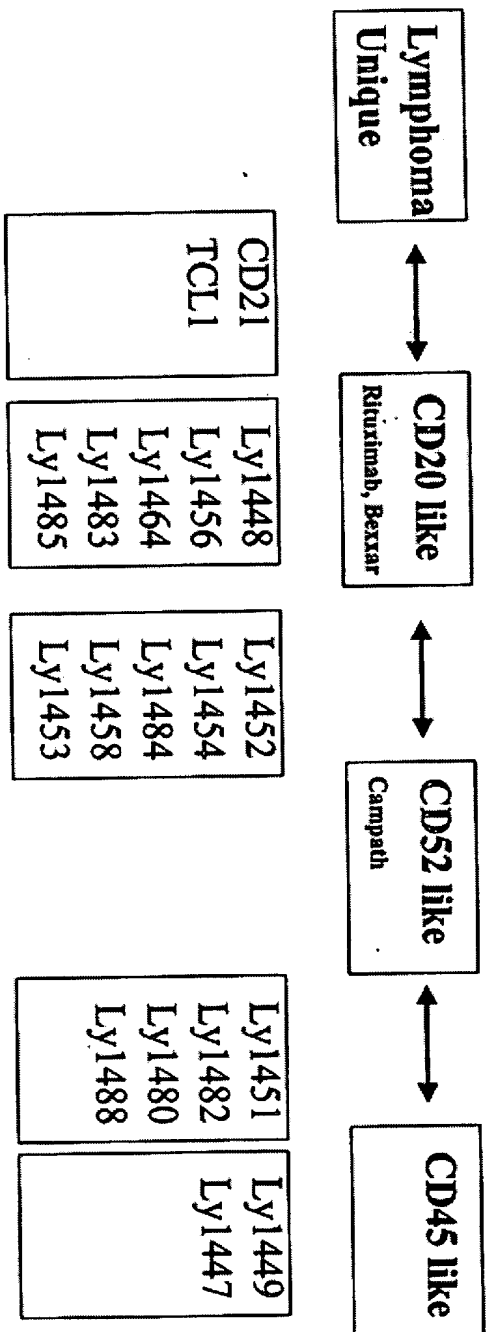
6/52

High Differential Expression in Group 1  
At Lymphomas > N comparison for Lymphomas  
Threshold : 3  
At Mean Signal > 0.3

Seq. Element (BP)	BP	Mean Signal 1	Mean Signal 2	Gene	Chrom	Start	End	Strand	Score	Score	Score	Score
ID No. a.1												
10,548 R0410 D9	389	40.12	0.207	0.006	0	0	21 (9704428)	3	0	3	0	0
10,552 R0411 D1	274	37.21	0.406	0.111	1	0	57 (1325575)	1	0	1	2	0
10,574 R0442 H5	202	16.27	0.394	0.022	12	0	16 (6605577)	1	0	2	0	0
10,553 R0413 B9	509	13.46	0.368	0.027	0	0	37 (10559002)	1	0	1	1	1
10,547 R0410 D5	332	12.1	0.455	0.036	7	0	60 (4783542)	1	0	1	0	4
10,561 R0432 A11	729	9.87	0.556	0.067	2	0	46 (11580335)	5	0	3	0	4
10,572 R0441 B1	502	8.79	0.673	0.089	178	0	34 (7986550)	8	0	0	2	2
10,553 R0417 C9	363	6.65	0.341	0.051	0	0	4 (1028308)	1	0	1	0	0
10,541 R0408 E10	319	5.33	0.332	0.062	7	0	159 (12604425)	4	0	3	3	3
10,562 R0438 B1	364	4.55	0.324	0.071	1	0	1 (7113300)	1	0	1	0	0
10,569 R0439 D6	471	4.4	0.38	0.062	12	0	14 (10399152)	2	0	2	0	0
10,551 R0410 C11	530	3.44	0.328	0.085	3	0	29 (1280008)	1	0	2	2	2
0.1 - 0.2												
10,576 R0457 A8	231	10.19	1.761	0.173	22	0	4 (12874085)	3	0	2	1	0
10,567 R0438 F6	465	7.78	1.6	0.193	33	0	1 (13290639)	1	0	1	0	0
10,565 R0439 C4	350	7.5	1.053	0.14	41	0	4 (5394077)	4	0	4	0	0
10,580 R0469 F1	653	6.82	1.03	0.161	25	0	98 (12525443)	3	0	4	1	1
10,545 R0410 A7	375	6.5	0.959	0.148	0	0	22 (1155912)	10	1	6	1	0
10,540 R0408 A1	233	4.97	0.612	0.123	7	0	10 (13129811)	1	0	1	0	5
10,560 R0428 D9	522	4.17	0.789	0.184	25	0	146 (14087353)	14	0	13	0	1
10,577 R0457 B7	453	3.97	0.47	0.118	6	0	0	4	0	5	1	0
10,556 R0418 A2	334	3.81	0.423	0.106	4	0	38 (12428993)	3	0	2	3	0
10,550 R0410 F10	298	3.9	0.435	0.112	3	0	4 (2984224)	1	0	1	0	3
10,543 R0409 B7	302	3.87	0.509	0.131	5	0	98 (12708451)	3	0	3	0	3
10,557 R0415 D12	546	3.85	0.418	0.108	6	0	38 (12945863)	13	0	13	0	0
10,544 R0409 D12	583	3.71	0.568	0.153	4	0	126 (12000010)	9	0	2	5	0
10,579 R0459 D2	342	3.66	0.513	0.14	1	0	83 (12787237)	9	0	8	3	0
10,563 R0438 C1	377	3.56	0.419	0.117	2	0	0	2	0	2	0	1
10,549 R0410 E1	358	3.48	0.347	0.1	3	0	35 (2910344)	4	0	1	1	1
10,559 R0417 E7	455	3.44	0.35	0.102	0	0	117 (12333953)	6	0	6	2	0
10,534 R0413 A5	364	3.4	0.345	0.128	0	0	19 (1359988)	8	0	4	0	0
10,538 R0407 B1	369	3.29	0.414	0.101	0	0	22 (8362795)	2	0	3	0	0
10,539 R0407 D4	188	3.17	0.321	0.101	8	0	59 (11681430)	1	0	1	1	1
10,566 R0438 F4	270	2.19	0.416	0.132	8	0	1 (12155867)	1	0	1	1	0
10,537 R0406 H8	662	3	0.321	0.107	3	0	32 (1137727)	1	0	1	1	0
0.2												
10,568 R0439 C11	678	13.02	3.704	0.285	51	0	7 (2004441)	1	0	1	2	0
10,546 R0410 B8	408	10.65	4.045	0.38	1	0	38 (10714462)	5	0	5	5	0
10,564 R0436 C10	467	7.79	1.95	0.35	45	0	239 (14055451)	8	0	5	5	0
10,570 R0440 E11	411	8.39	2.381	0.389	135	0	14 (12727100)	8	0	9	1	1
10,578 R0438 C7	430	5.36	3.701	0.69	0	0	0	101	0	100	0	0
10,573 R0441 B8	330	4.09	0.905	0.221	44	0	3 (2436300)	8	0	8	0	0
10,542 R0408 A3	588	3.69	0.757	0.205	10	0	31 (9857449)	2	0	3	2	0
10,538 R0417 C8	499	3.27	1.778	0.543	1	0	68 (12307281)	11	0	7	0	10
10,571 R0445 D10	305	3.26	1.865	0.602	42	0	119 (12784428)	11	0	9	0	0
R0440 H9	303	3.21	0.816	0.284	0	0	45 (2400828)	3	0	3	0	0

FIG. 6

# Hematology therapeutic Ab candidates

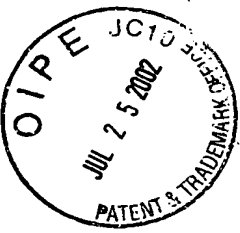


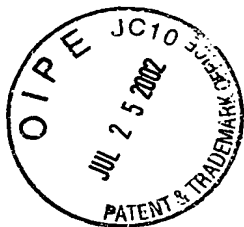
# Identification of lineage specific markers and candidate lymphoma, leukemia and myeloma antigens

Gene	CD34+	CD19+	CD14+	CD2+	Ly	Hodgkin	Myeloma	CLL <sup>+</sup>	AML
CD20	-	+++	-	-	+++	+	+	++	+/-
CD21	-	+	-	-	+++	++	+	+	-
TCL1	-	+	-	-	+++	+	-	++	-
Ly1448	-	+++	-	-	+++		++	++	-
Ly1452	-	+++	-	-	+++	+	+	++++	+/-
Ly1456	-	++	-	+	++ T-NHL	+	++	++++	-
Ly1464	-	+++	-	-	+++	+	n.d.	n.d.	n.d.
Ly1483	-	+++	-	+	+++	++	+	n.d.	-
Ly1458	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
Ly1481P	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
Ly1485P	-	+++	-	-	++	-	n.d.	n.d.	n.d.
Ly1480	+	++	++	+	+++	+	n.d.	n.d.	n.d.
Ly1488	+	++	++	+	+++	+	n.d.	n.d.	n.d.
Ly1484	+	++	+/-	+/-	+++	++	n.d.	n.d.	n.d.
Ly1482	++	+++	++	+++	+++	++	n.d.	n.d.	n.d.
Ly1453	++	++	++	++	+++ T-NHL	+++	+++	+++	+++
Ly1449	++	+	-	-	+	+	+	+++	++
Ly1447	++	+++	+	+	++	++	n.d.	n.d.	n.d.
Ly1451	++	++	-	-	++	+	+	++	++++
CD52	++	+++	++	++	++	++	n.d.	++	n.d.
CD45	+++	+++	+++	+++	+++		n.d.	n.d.	n.d.

\* single probe

Figure 8





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SER ID NO:

10,581

Lyl447 sequence:

CCITCAACAGACTGGATGGGGTCCACCCACATTAGGCTGGAGTTTGTCTGCCACTGTGCAGTTATCATTCTGGGATGGG  
GGTACCTTACTCTCCCAATGAGAAATTTCTAAATTTCTCTTTTGAGCCTGGTGCCTCCACCTTCTCANAACTGCATAGGG  
CGTGAGCTTTGTGTGGTATGTGACCTCCAGAACAGACTGTGAGCAGATTTTTTCTTTAATCTGAGCCTATGCTTGCTG  
CTGTCCTTCTTGACTTTCAACTAGGCCCTAAAAAAGCGN

SER ID NO:

10,582

Lyl448 Sequence

CCAGGGTTAGGACATTCAAATGTCTTTATCCACATTCTGGAAGGATAATTGTTATAGATTCCCTACCTCCATAGGAATGC  
TTATAATGGATTATCTATACAACTCCACATTCCACATTTTGCTTAGAGAAATGGAATCAGTCAAACCTGTGCCAGA  
GTTTCCCTTAGAGTTCTCACCTGTTGTCTTATATCCATCTAGGAATCCCATCTCTAATGTAAGCTTGGAGATCCGGGCC  
CCCGGGGACAGGTGACTGAAGGACAAAACTGATCTGCTCTGCTCAGTGGCTGGGGGTACAGAAATGTCACTTCTC  
CTGGTACAGAGAGGCCACAGGAACAGTATGGGAAAGAAACCCAGCGTTCCCTGTACAGCAGAGCTGGAGATCCAGCTG  
TGAAAGAGAGTGTGCGGGCAAATATTACTGTAGAGCTGACAACGGCCATGTGCTATCCAGAGCAAGGTGGTGAATATC  
CCTGTGAGAGACCTGATGGCTATAGAAGAGACCTCATGACAG

SER ID NO:

10,583

Lyl449 Sequence

CCACATTGGGAATTTGTCACACAGGTGCTGCTCCACCANNCAGAGAGGCTCAGGAGATTGTCCAGGGACAAGGAGACCT  
GGCCGGACCTCTGCGAGGAGGTGAGGCCCTGCCCCATCTTGTCCTCATCATTCTGGATGTTGGCATCCOCAGGCTC  
CTGGGAGGGGAGAGTGTCTGATAAAAGGCCAAAAATCACACAGAAAGAGACAGAAAACTCCAGCCTTCTTACATAG  
GTGCTACCGTATTCTACGAGCACGGGGCTGTGTTGAAGACTCCCTCTGGAAGTTACAGAAAGGAGCCACAGAGTTT  
AGCCTCACGCTCTTTCTCAGATGCAGTCAACACTTTACCAAACTTGGCACATCCAACTCTTTTCAATTTTACA  
CCTGTTTGTGGCTGCTGACAGATATTTGTNATTGATCTTTCTAATTTACGGGATTCTAAATGTGTTTGTAGAATCTG  
GTCAGCACTCAGGATTCTGCTTT

SER ID NO:

10,584

Lyl451 Sequence

CTGCTGCTAAATACCTMTGAGAACTCTGCTTCTATCTAAGGGGACCTACTTTTNTCNGGAATCTCAATACTTGGAAACA  
GAACCTCTTANACGGACCTTTGGCATATGAATTTGGACCACTGTAGGTTCCAGGACTAGAGAGCCAGCAATGCTCTCA  
TGAACAATCTCACCAATTACTCTGCTCAGGAAACGAGGTAACCTGATGGACAGCCGAGGCCCTTAGGGCGCTTAGG

SER ID NO:

10,585

Lyl452 Sequence

AAANACCAATAGCAGCCAAAACAGAACTTTGTAAACAAAACCAACTATCAGCCCTGTGCTTAAACACAGAACTGCG  
ATTCTTTTGAACATTAAGTATATGCAATAAGAGAAATAGAACATCTTTTCTTAAATATACATACCAATATCTAA  
AACAAATGTCACCAATATAGACACAAATCGGTGTTATCATAGGCATGTTGAACAGTCTTTTTCACAGTACTCAGGGGCA  
TCATGGGGCTGCGAGGGCCACACTTTCCAGAAAGTTTCTCTGCTGCTGATCCTGCGCACCCCGGGGCACTCGGAGGACT  
GGAAGCACTGTTTGTGAAAGCAAGCCCTGCAAGCTGAACATCTTCTACATGTTGCTGTCTGAAATGGGAGATGACAGTC  
GTATTCTGGCAAAATTCACAAATAAGCCCTTTCTCTGACACAGCTCACAGCCAGCCACATGTGCAAGGGAAGCTTGNAG  
AATGCTCTGAGTAAGGGTCCAGCAGCCCTTTCTTGTATCTGACAGGCTCCTCAAGGGAGAACAGGTGGAGCTCATCAG  
TCAAGTGTCCCGCCCTGCTCACAACTCTTTAATGCACTGTTAGCAAACTACAGGCTCTTCAACAGCTTCTTGATAT  
GGAAGAGCTGCTCTGAAATTTCTTC

SER ID NO:

10,586

Lyl453 Sequence

CCAAAAAATTCAGCATAAAACTATCCTGCTGTGATTATATATATTTATTACNNNATTTAATAAACAACCACTTT  
TGAACCAAGTAATTTTATCTAGTGTGAAAGAAATTAATCACATGGTCTATATACTGGCTAGTGTCTCTTAAAAGTAGACA  
TTAAATATTTTCAATTTGAGGGAATCTTTGGAGATTAGTGGCATCTAATCTTGGGGCTCAGACACCCAAATCTATA  
TATTGACAGTGGAAAGTTGATGATTGTTATCAAAATTCAAAGCACCTAATGGAAACCCCACTTCTCTGTGAAGATT  
TTCACTGCTTTACAGTTATTTGAAATTTTCAATTTCTGTGAGGCCACTTCAGAACTCCAAATGGGCTTTGCAATATT  
AAATGTGGAGAAATGCATTAACTATTATTAACTCAATGAGTTT

SER ID NO:

10,587

Lyl454 Sequence

CCTCTCCACAGGCTGCTTGAGTGTCTCATGACACAACAGTTGGCTTACTCCAGAGTGAGCAACTCAAGAGAGAGCAAGG  
CAGAAGCTACCAATCTTTATGTTTGAAGTCATGCACCATCTTTTCAACAGTATCTGTTGATTATTTTGTATCAGCTTG  
TTCACTGTGGAGGGAATTCACAAGGGCATGAATACTCCACTGGCAAGGATCATTTGGGGCCATCTTGGAAAGCTGTGTG  
AATGAGCAATGAATGCCACATAGAAATATTAGCAGTGCAATGATGCTAGAGGTCACTACCCCACTGTCTCTGTGCTC  
TTCTCCCCAACCCCTCCCTGCTCCAGGCAAGAGCCCTTAGCCTCTGCTGATCACTTTCAAGCACTCAACATCTTCA  
GGGAACCTATTCCGCGTGGGACAGTGTAAATAGTGGAAAACTCTTTTCAAAAGTTGAAATCAGTTCTCTGTGTCTTA  
TTACCTGCTGATCACTGTCCAGACTTCTGGAGGACACAGAGCAAGTTTATTCTCTTACTGATGTTAGCTTTTCAATC  
CATCCCTTCCCTCCAGTATATTAGAGTTACGTAATTTCTAAATGCTTAGCAGCTCATTTATCTGAAACA

SER ID NO:

10,588

Lyl456 Sequence

AAAGACATGAAAAATATCCCAAGATCATACTAGATCATAATAGCAATTCCTTTACAAATGAATTTAGGAGTAACTGATC  
TCTAACAGTTTCTTTCATGTTGTTTAAATGCAAGGGCAGAGGATCTGCGACCTTGGAAACAGCGTGAGCTAACCCAC  
GTGCTATAGACACTTCATGTTGCTTACCCAGGGAGTCAAAGCGCTTTGCTCCCTCACTGTCTGTGAGTCTCAGGCCAT  
TAGTAGCCACCCCGCTGCTCCAAACTTGAAGTTGTTTCAAATGTTTCTCACTGTTTCACTCTCTNCACTGACCCCACTC  
CAGAAAGCTGGAGAGAGGCCAAGATGCCACCCACTTCCCAATCCCTCGCCACAGATCTGTGCTATCAACACTCTG  
TAAAGTGCCTTTGCTTCTCTCTTGAAGAGACTGAGAACACACATTTAATGTTTAAAGAAATGGGGCAGGCTAA  
AAATGACTGATCCCAACCGCAGTGACTCA

SER ID NO:

10,589

Lyl458 Sequence

TTGAATGCTCTATTTTGCNNNTAANNNTTATTNACTAGTCTCAGTAATACATTAGTAAAAANCATGTGCTTAAATTAAT  
GGGTTANAATCAANAACATANAAGTGGGCAATATACCTTNACTCCCATCCCACTCCCAATCTTACTCTACTCATNTC  
ATTCTCATTAATTTGGGAAANCATNANAANATGGGTTGCTTGAAGTAANANATTAANAANAATTAAGCTTTTGTATCCCTG  
CCAAACCCCATGCCAGGGGGGNCACCTTCAATCAATAACATGCCAGGAANAGTAAGNTGCCCTTCTGANGCCGNA  
ATCTGCCATCATNTTCCATNTTCCAGCTNTTCCATTTGTCNAGNCAATCTGGGCTCTCAGGATNATACCCGGTCTTA





**G**

**Ly1464 Sequence**

aaagagaactaatggaagtggattgaatacagcagctctcaactgggggcaattttgcccc  
ccagaggacattgggcaatgtttggagacattttgggtcattatacttgggggggttggggg  
atcgtgggatatgtgtg

Ly1480 Sequence  
CTGTAGCCTCTGCAAGTGA AAAATCCAGGCCGACTTGCAGTCATTGGACTGATGTCCAAGTGC AATCACCATACAGCAGCT  
ACAGGCAAGGGCTGGCTGATAGGGAGTATGGGAGAAAGGACACGCTCAGATGAAAAATGCATGCATGCAACGATTTTCACCACTG  
AACACACTGTTTCTGTGATAGAACTGTGGCCCTGTGGGGGACAGATATTACCGBCTCTACTGAGCCAGTGGATGATGC  
CACCAAGGGCGGGCTGCCCTGTGATGTCCTCTTTACCTCTAAAGAAAGGACCATTAAGGTAAAAGGCGACCTACCTTATGTG  
AGTGAGCCCCAGACCCAGGGA AAAAGCTTGGGTAGAA CAATCCAAGGGGCAGCCTGGGTGTGAGAAATCCAGCCC AAGCTAG  
CTGCTCTAGAAAGCTGGAGG

**Ly1482 Sequence**  
 AAAAACCAATCTACAGGCAGTTCCTTTACAAGTCTCATATTTACAGATAGCACAAAGCTATGGCATGGCGTATGGCCTCCCTC  
 CTAATAATACAGATTCTTTGGCATATTTGGAATTGGTCAGCCTCAAAGACGGGCTGGCTACATCGTGCACGAGACAGTCCC  
 GCTTATTCCTCGTACAGGAGCTCGGAGACGGTCTCTAGCGGGAGGAGCTCAGGTCCTCCCTGGCCGACACAGCTGCCCCAGA  
 GAGTCCTCCGACGAAGCATGGACAGTTCTGCTCTGTTCCATCGCTCAGGCAGGGGAGAGAGTCCGGTGG

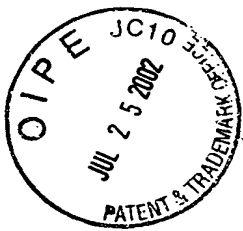
**Ly1483 Sequence**  
 GCTGGAGTCTCACTGTGAGTCCCTGAGAGGCTCCTTCCCGATCCTGTACTGTTTATCACGAGGATGACACCTTGGGGA  
 ACATCTCGGCCCACTCTGGAGGAGGGGATCCTTCAACCTCTCTCTGACTACAGAACATTCTGGAACACTACTCATGTGAG  
 GCTTGACATGGCTCGGGGGCCAGCAGTAAGTGGTGACACTCAATGTTACAGGAAGTCCAGGACAGACAGACAGGCC  
 TTAACCTGCGGGAACTACGGGGCTGGTGTTCARCATCTGCTCGTTGCTGCTGCTGCTCTGCTGCATTACGCAGGG  
 GCCCGAAGGAAACAGGAGGACTTCTGCCACTGGAAACATCTAGTCACAGTCTTAGTGAGTGTGAGGAGCCTTCTCTG  
 CAGG

Lyl1484 Sequence  
 CTGGGCGATCAACCAAGTTCACAGTTCCTCCAGCGTGCTGCTCAGCCCTCCGAGTGTGTGTGCTCATCTCTTTTCATAGAAGTCCC  
 ATCGGGCATGGAGAGGGTTGGGCTGCAGAGCTGTGATTTGCCAGAGGGCCCTTCTCTGAGAACTGTGGGGAAGGAGGCCCTG  
 GGGGTTTCTCTCTGATGGCAGAGCTCAGGCCCAAGTCACTCTGCCAACCTCAGCCTGGCACTGTGTGTCACAGAGCCCTG  
 CTGCTCTCTCTTGTACCATCTGCGACAGCAGACAGATATCTCTCCCTCTCATCAACCAACGAGGAGTTTGGTGTGGTT  
 TCTGGACAACCGCCAGAGCAGGTCACTCGGGGGCTGGTTTGTGCGGGCTTCCCTGTCAAAAGCAATGTAAAGCTCAGCCTGT  
 CGACTCAAGGCGCAGGTTCTTCTCCACTTGTGGCTCTTGGGCTTGGAGGCTGAGCCAGGGGCTCTCTCTCTGCTGGCCG  
 TCCAGGAACAGGACATCTTACATCTCAGTCTTCCAAACCGGACCATGCGCTTGAATCTCCGGTGGATGATGATCTGG  
 CTGTGTCTCCATCTCTGGGCGCTCATACAGGACGACAGATATGCTGCTCTCTGGGCGCCAGGCTGTGGTATGATCTGG

**Lyl1485**  
 CTGTCCTCCACTGCTGGAGTTACTATTTTTCTCTTTTCCCATTTTTATTTCATCAGAAGCCAGTCACTAAGCGAGGTCAAACTC  
 CAGGACAGGGGAATTAAGTGCCACCTTCTGGAGAGGGAGCATTCAACATTTATTCTTGGGATCTTCTGTAAGGAAGAGC  
 TGTTTCTCTCTCAAAAAAATCTTTAACTCTTTTAAAGCCTCAATTTCTTAATTGTGAAATGGGGCTAATACCTGTATCCAA  
 CCAAGGGAGGTAGTTAGAAGGTAACATGATAGGTGGGAAAGCATTAAACATAGGCAAAATGTTATATCAGGAATGATCGAG  
 AGACCCATCTCAACTATCTGAGAGGAGTCACTTAATCTCTAGTCTCAAGCGCTGTAAAGTCTGCATCTTTCATCGGGG  
 GTAAAGGCCCCAGTCTCTGAGACGGGCGAGTTTGGAAAGACAGCGCTGGTTTTTCTCTGTTCTCTGAGAGCCCTTCAGA  
 TGAGAAGGGGAGGTCTGGAGACAGAATGCCAAAAGCCCATTAAAGGCCACGGCCTTGCATTTTCAGAGAGGGAGCAGGTCTAG  
 AAGAAGACCGAGGAGCTCAG

**Ly1488**  
 CTGGYCTGTGGGTGATCCCAGCTCTTACTAGGAGAGGGGAASTGAAGGTCYTGGTGCCAGGGGCCAGGGCCCTCCAAACCAT  
 AAACAGTCCAGGATGGAACCTGGTTTCAACCTTCATACCAAGCTCCAAGCCCCAKACCATGGGAGCTGTCTGGGATGTTGAT  
 CCTTGAGAACATTGGCCCTGTGCTTTAGACCCAAGGACCCGATTTCTGGGCTAGGAAAGAGAGAAACAAGCAAGCCGGGGCT  
 AACTGCCCCCCAGGTGG

**FIG. 9**  
**Page 2 of 2**



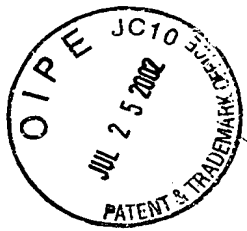
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Figure 1a. Lyl1464 full length DNA sequence (SEQ ID NO: 10,597)

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1 gatgcaagga gatgagacag ttaaattttac ttcctctttt ctaatctgag aggtttcatg
61 ttgaagaaaa tcagtgttgg ggttgcagga gacctaaaca cagtcaccat gaagctgggc
121 tgtgtcctca tggcctgggc cctctacctt tcccttggtg tgcctcgggt ggcccagatg
181 ctactggctg ccagttttga gacgctgcag tgtgaggagc ctgtctgcac tgaggagagc
241 agctgccaca cggaggatga cttgactgat gcaaggggag ctggcttcca ggtcaaggcc
301 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat cctccaaggt
361 ccagccaagc cagtttttga agggggacct ctggttctgc gctgccaggc ctggcaagac
421 tggccactga ctcagggtgac cttctaccga gatggctcag ctctgggtcc ccccgggcct
481 aacagggaat tctccatcac cgtggtagaa aaggcagaca gcgggcacta ccactgcagt
541 ggcactctcc agagccctgg tccctgggac ccagaaacag catctgttgt ggctatcaca
601 gtccaagaac tgtttccagc gccaatcttc agagctgtac cctcagctga accccaagca
661 ggaagcccca tgacctgag ttgtcagaca aagttgcccc tgcagaggtc agctgccccg
721 ctcctcttct cttctacaaa ggatggaagg atagtgcata gcagggggct ctctcagaa
781 ttccagatcc ccacagcttc agaagatcac tccgggtcat actggtgtga ggcagccact
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961 gctcctgagg agggccctgg gcctctgcct ccgcgcgcaa ccccatcttc tgaggatcca
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1141 ttatctggcc accggaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt
1201 catccatgat ctcacttaac caccccaata aatctgattc tttattttct ctctcttccc
1261 tgcacatatg cataagtact tttaacaagt gtcccagtg tttgttagaa taatgtagtt
1321 aggtgagttg aaataaaatt atataaagtg agaattagag tttagctata atttgttatt
1381 ctctcttaac acaacagaat tctgctgtct agatcaggaa tttctatctg ttatatcgac
1441 cagaatgttg tgatttaang agaactaatg gaagtggatt gaatcacgca gtctcaactg
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2041 agatgacatg tatgagaacc aaaaaacagc tgtcgccaaa caccgactct gtcgttgct
2101 tgatcttgaa cttccagcct ccagaactat gagaaataaa attctgttgt ttgt
```

Figure 1b. Lyl1464 protein sequence (SEQ ID NO: 10,598)

```
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SAEPQAGSPMTLSCQTKLPQRSARLLFSFYKDGRIVQSRGLSSZFQIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSA
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TAE
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## TMpred Report for Ly1464

Date:

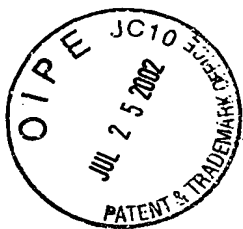
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PGTTKATAE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1464 has 358 amino acids and 3 Transmembrane Domains

Transmembrane Domain 1:	3 - 24	Score: 1.5484
Transmembrane Domain 2:	71 - 92	Score: 1.3009
Transmembrane Domain 3:	158 - 179	Score: 1.3027



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**Ly 1464 MHC class binding peptides (SERIDNDs: 10,599-10,819)**

**Ly1464 A1 binding peptides**

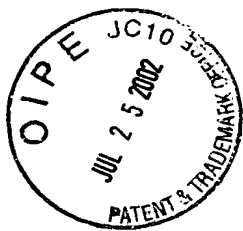
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	90
2	ASEDHSGSY	230	67.5
3	FSEPFHLIV	67	67.5
4	LTDAREAGF	52	25
5	SSEDPGFSS	300	6.75
6	ELFPAPILR	167	5
7	SSEFOIPTA	222	2.7
8	MPDPHLYHQ	312	2.5
9	LMELRELSG	339	2.25
10	HTEDDLTDA	47	2.25
11	CTEESCHT	40	2.25
12	ALGPFGFNR	118	2
13	LGMDDPHLY	310	1.25
14	CVLMAWALY	5	1
15	KADSGHYHC	135	1
16	LRELSGHRK	342	0.9
17	QLEIRVQGA	255	0.9
18	WCEAATEDN	239	0.9
19	SAEPQAGSP	179	0.9
20	AREAGFQVK	55	0.9

**Ly1464 HLA A2 binding peptides**

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLSLGVLVV	13	4047
2	LLLKHMODV	323	1006
3	VLMAWALYL	6	739
4	VLWVAQMLL	18	301.4
5	MLLAASFET	24	271.9
6	ILQGPAPKV	81	118.2
7	LLGHLLMEL	334	83.53
8	LLAASFETL	25	33.81
9	WQDWPLTOV	102	29.84
10	YTFSEPFHL	65	29.29
11	LIVSYDWLI	73	18.29
12	KLPLQRSAA	195	17.39
13	WALYLSLGV	10	16.44
14	CQAWQDWPL	99	16.24
15	GIPETASVV	153	16.08
16	QVWKQSPQL	248	15.51
17	ALYLSLGVL	11	8.38
18	QMGLLLKHM	320	8.252
19	VVAITVQEL	160	7.309
20	GVLWVAQML	17	6.916

**Ly1464 A3 binding peptides**

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	WLILQFPAK	79	30
2	ELFPAPILR	167	18
3	ALGPFGFNR	118	9
4	VLWVAQMLL	18	6
5	VLMAWALYL	6	5.4
6	LLKHMODVR	324	4
7	KLGCVLMAW	2	2.7
8	PMTLSCQTK	187	2
9	LLGHLLMEL	334	1.8
10	GMPDPHLYH	311	1.8
11	PLTQVTFYR	106	1.8
12	LLAASFETL	25	1.8
13	HLYHQMGLL	316	1.35



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14	ALYLSLGVL	11	1.35
15	YLSLGVLWV	13	1.2
16	ATEDNQVWK	243	1
17	HMQDVRVLL	327	0.9
18	HLIVSYDWL	72	0.9
19	KAYTFSEPF	63	0.9
20	KQSPQLEIR	251	0.81

Lyl464 A11 binding peptides

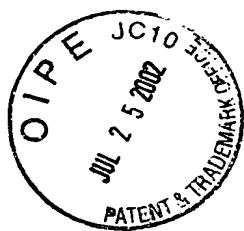
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1	ATEDNQVWK	243	1
2	WLILQGPAK	79	0.6
3	KQSPQLEIR	251	0.36
4	CQTKLPLQR	192	0.24
5	RVLLGHLLM	332	0.18
6	PTLNPAPQK	270	0.15
7	ELFPAPILR	167	0.096
8	ARLLFSFYK	203	0.09
9	GVLWVAQML	17	0.09
10	LLKHMQDVR	324	0.08
11	ALGPPGPNR	118	0.08
12	GHRKPGITK	347	0.06
13	RVQGASSA	259	0.06
14	LPLQRSAAR	196	0.06
15	BFSITVVQK	127	0.06
16	YTFSEPFHL	65	0.06
17	ITVQELFPA	163	0.045
18	YHQMGLLLK	318	0.04
19	QVWKQSPQL	248	0.04
20	LFSFYKDGR	206	0.04

Lyl464 A24 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LYHQMGLLL	317	200
2	VFEGLDLVL	89	30
3	TFYRDGSAL	111	20
4	GFQVKAYTF	59	15
5	KPVFEGDLL	87	12
6	HMQDVRVLL	327	10.08
7	GVLWVAQML	17	10.08
8	LYLSLGVLW	12	9
9	IFQSPGPGI	146	7.5
10	APREAPGPL	285	7.2
11	TFSEPFHLI	66	7.2
12	HLLMELREL	337	6.6
13	MTLSCQTKL	188	6.6
14	VLMANALYL	6	6
15	HLIVSYDWL	72	6
16	GCVLMAWAL	4	6
17	LLGHLLMEL	334	5.28
18	VVAITVQEL	160	5.28
19	MAWALYLSL	8	4.8
20	DVRVLLGHL	330	4.8

Lyl464 A68 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ELFPAPILR	167	45
2	ATEDNQVWK	243	30
3	ELRELSCHR	341	22.5
4	DVRVLLGHL	330	18
5	ALGPPGPNR	118	15
6	LPLQRSAAR	196	10
7	ETLQCEGPV	31	9
8	RVLLGHLLM	332	8
9	VVAITVQEL	160	8
10	VVAQMLLAA	20	8



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11	GVLWVAQML	17	8
12	KQSPQLEIR	251	7.5
13	PTLNPAPOK	270	6
14	AVPSAEPQA	176	6
15	ETASVVAIT	156	6
16	VVQKADSGH	132	6
17	WLILQGPAP	79	6
18	LLKHMQDVR	324	5
19	CQTKLPQOR	192	5
20	RVQGASSA	259	4

Lyl464 B7 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	200
2	KPVFEGDLL	87	80
3	APBEAPGPL	285	72
4	LQSAARLL	198	40
5	QVWKQSPQL	248	20
6	VVAITVQEL	160	20
7	IVSYDWLIL	74	20
8	GVLWVAQML	17	20
9	VLMANALYL	6	12
10	MANALYLSL	8	12
11	ALYLSLGLV	11	12
12	HMQDVRVLL	327	6
13	APGTAPEEA	281	6
14	SPMTLSCQT	186	6
15	DAREAGFOV	54	6
16	RVLLGHLIM	332	5
17	HLLMELREL	337	4
18	LLGHLLMBL	334	4
19	VLWVAQMLL	18	4
20	HLYHQMGLL	316	4

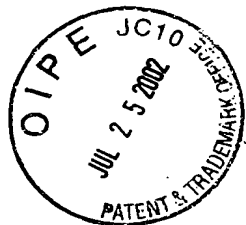
Lyl464 B8 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	8
2	DAREAGFOV	54	7.2
3	LQSAARLL	198	1.2
4	PSFYKDGRI	207	1
5	GCVLMAVAL	4	0.8
6	MANALYLSL	8	0.8
7	LLGHLLMBL	334	0.4
8	HLYHQMGLL	316	0.4
9	VLMANALYL	6	0.4
10	AARLLFSFY	202	0.4
11	APILRAVPS	171	0.4
12	ALYLSLGLV	11	0.4
13	HLIVSYDWL	72	0.4
14	LLAASFETL	25	0.4
15	VLWVAQMLL	18	0.4
16	HMQDVRVLL	327	0.3
17	APBEAPGPL	285	0.24
18	LSGHRKPGT	345	0.2
19	GVLWVAQML	17	0.2
20	SSSAAPPTL	264	0.2

Lyl464 B27 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LRELSGHRK	342	2000
2	VRVLLGHLL	331	2000
3	ARLLFSFYK	203	2000
4	AREAGFOVK	55	2000
5	QRSAARLLP	199	1000

FIG. 12  
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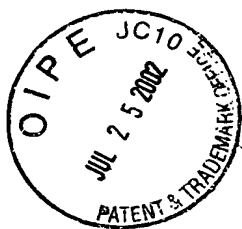
6	GRIVQSRGL	213	600
7	NREFSITVV	125	600
8	KQSPQLRIR	251	300
9	HRKPGTTKA	348	200
10	IRVQGASSS	258	200
11	COAWQDWPL	99	200
12	LRCQAWQDW	97	200
13	HLYHQMGLL	316	150
14	ALVLSLGVL	11	150
15	VLWVAQMLL	18	150
16	CQTKLPLQR	192	100
17	VQKADSGHY	133	100
18	LQGPAPKPVF	82	100
19	AQMLLAASF	22	100
20	KAYTFSEPF	63	75

Lyl464 B35 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KPVFEGDLL	87	60
2	WPLTQVTFY	105	40
3	EPFHLIVSY	69	40
4	TPSSEDPGF	298	30
5	GPPGPNREF	120	20
6	AARLLFSFY	202	18
7	QSRGLSSEF	217	15
8	APPEAPGPL	285	12
9	VQKADSGHY	133	9
10	ASEDHSGSY	230	6
11	KAYTFSEPF	63	6
12	EAGFQVKAY	57	6
13	SSSAAPPTL	264	5
14	LSCQTKLPL	190	5
15	SSCHTEDDL	44	5
16	AATEDNQVW	242	4.5
17	KPGTTKATA	350	4
18	RVLLGHLLM	332	4
19	FPAPILRAV	169	4
20	DAREAGFQV	54	3.6

Lyl464 B44 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LEIRVQGAS	256	30
2	WPLTQVTFY	105	27
3	SEDHSGSYW	231	24
4	REAGFQVKA	56	18
5	EAGFQVKAY	57	13.5
6	LGMPPHLY	310	12
7	SEFQIPTAS	223	12
8	AEPQAGSPM	180	12
9	QELPPAPIL	166	12
10	SEPFHLIVS	68	12
11	SAARLLFSF	201	9
12	VAITVQELF	161	7.5
13	ASEDHSGSY	230	6
14	AARLLFSFY	202	6
15	DDLTDARBA	50	4.5
16	FSITVVQKA	128	3.375
17	EPFHLIVSY	69	3
18	AQMLLAASF	22	3
19	TEDNQVWKQ	244	1.8
20	CEGPPVCTEE	35	1.8



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# ANALYSIS RESULTS OF THE PROGRAM TSITES.

.....

These are the results of the analysis of the file --> LY1464-1.TXT

Beginning with residue: 1 and ending with residue: 359

AMPHI Window size: 11

A - AMPHI mid points of blocks.

R - Residues matching the Rothbard/Taylor motif.

D - Residues matching the IAd motif.

d - Residues matching the IEd motif.

SEQUENCE:  
10,518

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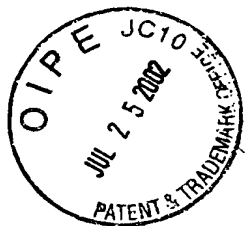
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KADSGHYHCSGIFQSP

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R.....RRRR..  
.....  
.....

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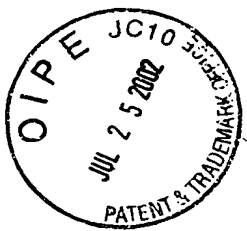
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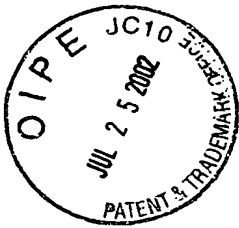




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Table 4. Immunogenic portions of Lyl464 (SEQ ID NOs 10,820-10,842)

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VVRVLLGHLLMELREL SGHRKPCTTATAT



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Ra12-LY1464 profile

CORIXA CORPORATION  
Antigen Discovery**LY1464 and recombinant Ra12-LY1464**

**Researcher:** Alex Gaiger, Aijun Wang, Jonathan Clapper  
**Reference:** cloning bk813 pg150, 151, 154-157; expression bk966 pg2-3

**Description:** LY1464 is an antigen discovered by Lymphoma program. The full-length sequence was cloned through PCR amplification of normal tissue cDNA known to express the gene. The gene was cloned directly into the pCRX2 vector as an N-terminal Ra12 fusion, **Ra12-LY1464**, using restriction enzymes Nco I and Xho I, and the sequence was subsequently confirmed. The optimal protein expression conditions were determined by mini-induction screening.

**Protein Diagram of Ra12-LY1464****Cloning Strategy:**

Tumor and normal tissue derived cDNAs (from Alex Gaiger) were each used separately as templates in PCR amplification reactions with two primers (LY1464-sense and LY1464-antisense) flanking the 5' and 3' ends of the gene LY1464. As shown below, the primers contained short 5' restriction enzyme recognition sequences. The PCR products were separated on agarose gel and the DNA band of ~1080bp was gel purified. This 'insert' was digested using restriction enzymes Nco I and Xho I and ligated to pCRX2, which was linearized with the same two restriction enzymes and then dephosphorylated. The vector and insert were combined in equi-molar ratios with DNA ligase to create a completed plasmid construct pCRX2 **Ra12-LY1464**. This ligation mixture was used to transform competent *E. coli* Novablue cells. Ten individual colonies from both tumor cDNA derived and normal cDNA derived construct were picked for DNA miniprep. Miniprep samples were screened for insert through restriction enzyme digestion (Nco I, Xho I) and five positive samples were sent for DNA sequencing. Miniprep clone #4 (Corixa seq ID#90522) was confirmed and used for expression of recombinant **Ra12-LY1464** in *E. coli*.

**Cloning Primers:**

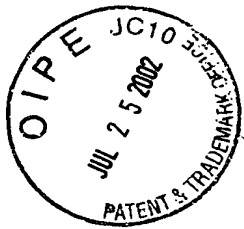
**LY1464-sense**  
5' - CGTCCATGGACatgaagctgggctgtgtcttc - 3' (SEQ ID NO: 10,843)  
prime 21bp 57%GC 56C Tm  
full length 32bp 59%GC 68C Tm

**LY1464-antisense**  
5' - CCTTCTCGAGctattcagcagtagcctttgtggtc - 3' (SEQ ID NO: 10,844)  
prime 25bp 48%GC 58C Tm  
full length 35bp 51%GC 67C Tm

**Protein Expression:**

Various *E. coli* strain/culture conditions were screened for optimal expression conditions for recombinant protein expression. Briefly, the expression construct was used to transform different expression hosts, and then mini-induction cultures were screened at varied culture temperature, culture media and/or IPTG concentration. The optimal expression condition was determined by evaluating the results of SDS-PAGE and western blot.

For **Ra12-LY1464**, The most optimal expression condition is pCRX2 **Ra12-LY1464** in Tuner (DE3) CodonPlus-RP grown in 2xYS media at 37°C induced with 1.0mM IPTG at 25°C (room temp) for 3hr.



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Ra12-LY1464 profile

CORIXA CORPORATION  
Antigen Discovery**DNA/Protein Sequence:****LY1464 (DNA) 1080bp (SEQ ID NO: 10,445)**

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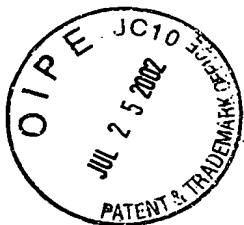
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**Ra12-LY1464 (protein) (SEQ ID NO: 10,448)**

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AE.

**Protein Info:****Ra12.LY1464**

Molecular Weight 53010.15 Daltons  
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29 Strongly Basic(+) Amino Acids (K,R)  
46 Strongly Acidic(-) Amino Acids (D,E)  
174 Hydrophobic Amino Acids (A,I,L,F,W,V)  
128 Polar Amino Acids (N,C,Q,S,T,Y)  
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-14.119 Charge at PH 7.0

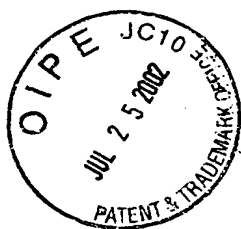


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1484  
Lyt448. DNA Sequence (SEQ ID NO: 10, 846)

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FIG. 17  
Page 1 of 2



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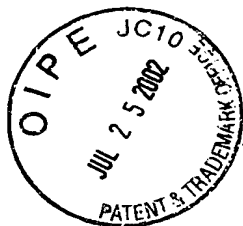
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**Ly1484. Protein sequence (long)** (SEQ ID NO: 10, 847)

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**Ly1484. Protein sequence (short)** (SEQ ID NO: 10, 848)

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LHRKALESDFVSANLHHWIDLIFGYKQGGPAAVDAVNI FHPYFYGDRMDL  
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## a. TMpred Report for Ly1484 Long

Date:

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GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG  
EPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTS PAVTALAVSRN  
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Black = intracellular, Red = Transmembrane, Blue = Extracellular

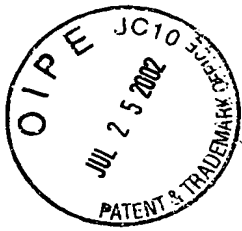
Ly1484 Long has 1269 amino acids and 5 Transmembrane Domains

Transmembrane Domain 1:	63 - 84	Score: 1.36675
Transmembrane Domain 2:	118 - 139	Score: 1.38695
Transmembrane Domain 3:	480 - 501	Score: 1.36185
Transmembrane Domain 4:	562 - 583	Score: 1.31785
Transmembrane Domain 5:	725 - 746	Score: 1.3521

## b. TMpred Report for Ly1484 (short)

MLQKWQKRDISNFEYLMYLNNTAAGRTCNDYMQYPVFPFWVLADYTTSETLNL  
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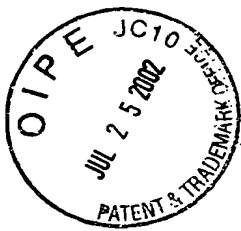
Black = intracellular, Red = Transmembrane, Blue = Extracellular



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Lyl484 has 646 amino acids and 1 Transmembrane Domains  
Transmembrane Domain 1: 102 - 123      Score: 1.3521





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Table2a: Ly1484 long MHC class I binding peptides  
(SEQUIDNOs: 10,849-10,908)

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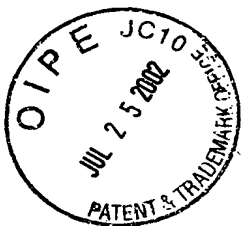
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	FLCLMHCL	145	836.3
2	YLPEFLTNC	783	818.9
3	KLYSGMPSA	57	742.3
4	FILEHIMVV	73	629.3
5	TLYSSLNKV	95	511.9
6	FLQEHMDVV	127	448
7	ILWDLHLT	1093	431.1
8	ALQGSFDV	743	403.4
9	MQYFVPPWV	654	400.9
10	ALYGHQAV	1063	222.6
11	YLVRMPPT	730	188.5
12	CLMHCLLL	148	181.8
13	GLLSILQFL	120	130
14	VIMTFENLA	1010	118.7
15	ILAVERNKV	973	118.2
16	YLASEKSL	260	98.27
17	ELTPEFFYL	776	97.11
18	YLMYLTAA	638	84.56
19	ILLFILEHI	70	73.96
20	LLQDIALEI	563	72.72

HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KMPGRQAK	292	135
2	VLLPFLWNR	981	60.75
3	CLGSYGSDK	1001	60
4	KVILYCLSK	102	54
5	CVWELSMTK	1044	30
6	LLFGHQHY	495	30
7	PLWEETMLK	247	30
8	FLSPHEDVK	180	30
9	SLYKDHVQR	326	20
10	FLVFYNDR	580	18
11	KLYSGMPSA	57	13.5
12	GLRLRQALY	1057	12
13	NLANPKIFR	672	12
14	RVMKTEDVK	1183	10
15	QVPRQLFTK	894	9
16	RMPPFTQAF	733	9
17	KLKFIQRPK	694	9
18	RIMLQKQK	622	9
19	VILQELLQK	465	9
20	IMLQKQK	623	6

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	655	300
2	FYICENFTL	502	300
3	TYNSNISFL	138	300
4	NYRRRGOEL	315	264
5	DYTSETLNL	665	200
6	SYLVRMPPF	729	150
7	RYPGSDRIM	616	75
8	RPLLQDIAL	561	60
9	LYSSLNKVI	96	60
10	YTHYSSAI	717	50
11	PPFALHESL	443	36
12	NFGQVFKQL	891	28
13	SYGSDKVLN	1004	25
14	GFDDFSCCL	994	24
15	EFFYLPEPL	780	24
16	YFYGDRMOL	865	20
17	SFCSFQPSL	594	20
18	RGLRLRQAL	1056	17.28
19	RQELYASL	319	17.28
20	KNLALSREL	1217	15.84



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CID1096 Table 2b.Lyl484 short MHC class I binding peptides  
(SEQ ID NOS: 10,901-10,968)

## A2

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLPEPLTNC	160	818.9
2	ILWDLHLT	470	431.1
3	ALQGGSPDV	120	403.4
4	MQYVFPWV	31	400.9
5	ALYGHQAV	440	222.6
6	YLVRMPPT	107	188.5
7	VLMTFENLA	387	118.7
8	ILAVERNKV	350	118.2
9	ELTPEFFYL	153	97.11
10	YLMLNTAA	15	84.56
11	VLADYTSET	39	51.94
12	RMFHSVKST	131	45.8
13	SNFEYLYL	11	26.76
14	KVLMTFENL	386	22.54
15	LLPPLMRT	359	21.54
16	QLPTKHPA	275	18.38
17	GAHLSIMNV	507	16.66
18	WDLHLTHV	472	16.5
19	FISLARKAL	198	13.51
20	CILWDLHL	469	12.25

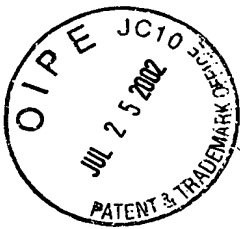
## HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	VLLPPLMNR	358	60.75
2	CLGSYGSDX	378	60
3	CVWELSMTK	421	30
4	GLRLRQALY	434	12
5	NLANPKIPR	49	12
6	RVWKTEDVK	560	10
7	QVPKQLFTK	271	9
8	RMPPPTQAP	110	9
9	KLKFIORFK	71	9
10	TILGFVSNF	261	4.05
11	SLPGHPQPF	301	3
12	WIDLIFGYK	218	2.7
13	NLJHMIDLI	214	2.7
14	YMQYEVFPW	30	2.7
15	ELTPEFFYL	153	2.43
16	ALYGHQAV	440	1.5
17	YLPEPLTNC	160	1.35
18	IIVASYLVR	102	1.2
19	DMTVQCHYY	87	1.2
20	QLPTKHPA	275	1

## HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYVFPWVL	32	300
2	DYTSETLAL	42	200
3	SYLVRMPPT	106	150
4	YTHYSSAI	94	50
5	NPGQVFKQL	268	28
6	SYGSDKVLH	381	25
7	GFDDFSCCL	371	24
8	EFFYLPEFL	157	24
9	YFYGDMDL	242	20
10	RGLRLRQAL	433	17.28
11	IGLALSRRL	594	15.84
12	KVLMTFENL	386	14.4
13	TFSWGFDDF	367	12
14	FYLPEPLTN	159	10.8
15	ANPKIPRDL	51	10.08
16	SFDVADRMF	125	10
17	KTSPAVTAL	614	9.6
18	KGRPRGLRL	429	9.6
19	RNKVLLPPL	355	9.6
20	EYLYMLNTA	14	9

FIG. 20



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ANALYSIS RESULTS OF THE PROGRAM TSITES.

.....

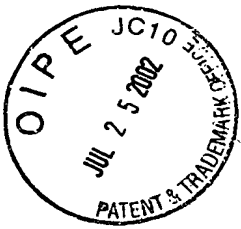
These are the results of the analysis of the file --> LY1484-1.TXT  
Beginning with residue: 1 and ending with residue: 1270  
AMPHI Window size: 11

A - AMPHI mid points of blocks.  
R - Residues matching the Rothbard/Taylor motif.  
D - Residues matching the IAD motif.  
d - Residues matching the IEd motif.

(SEND NO)  
19/8/97

```

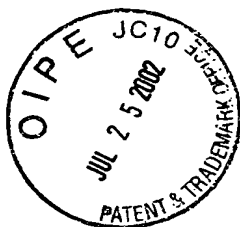
5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
RDPOSEVLLSAMELPHMTSGGDAAMPFRGKEPQPSABAAAAAPSLANISCTQKLVEKLYSGMFADPRHILLFIL
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....
.....DDDDD.....
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
EHIMVVIETASSQRTVLSTLYSLNKVILYCLSKPOQSLSECLGLSLILGLQEHWDVVFATYNSNISFLCLM
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....
.....DDDDD.....DDDDD.....
155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLILLNERSYFEGFGLSPKPMSTYHQVFLSPNEDVKEKREDLPSSLSDVOHENIQKTIVOTLMQOLVAQRQOTLED
.....AAAAA.....AAAAA.....
.....RRRRR.....R
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
APKIDLSVKPGEREVKIEKVTPLMEFTMLKAMOHYLAEEKSLASRSNVAHNSKVTLMWGSGLSSAMKLNPGROAK
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....
.....dadd.....
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEDFVSCIENYRRRGQELIASLYKDHVORRKOCHIKAAAMARIQEQLFGLGLWSQGBETKPCSPWELD
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....
380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WREGPARMRKRIKRLSPLEALSSGRHKESQDKNDHISQTHAENQDELTLEAEGSPDEVGVDCQTQLTFFPALHES
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....
.....dadd.....
455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHSEDFLELCRERQVILQELLDKEKVTQKPSLVIVQGHVSEGVLLFGHONFYICENFTLSPTGDVYCTRHLN
.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPPIFNLCSKORSTOHYSQOCHSYADMRELQARFLLQOIALEIPFHNGYSKFLVPFYNDRSKAFKSFCSFOP
A.AAAAAA.....AAAAA.....RRRRR.....RRRRR.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKGKATSEDTLMLRRYPGSDRIHLQKQKRDISHMPEYLMYLNLAAGRTCHNDYMQYPVFPWVLADYTSETLNLN
.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....
.....DDDDD.....
680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIPRDLSPKMGCAQTKERKLFQRFKEVEKTEGDNFVQCHYTHYSBAIVASYLVRMPPPTQAPCALQGGSPD
AAAAA.....AAAAA.....AAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....R
```



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.....DDDDDDDDDD.....  
.....ddd.....  
755 760 765 770 775 780 785 790 795 800 805 810 815 820 825  
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEPLTNCNGVEFGCMQDGTVLGQVLPWADGDPKRFISLH  
AAAAAAAAAAAA.AA.AAAA.AAAAAA.....AAAAA.....AAA.....  
RRRRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....  
.....  
830 835 840 845 850 855 860 865 870 875 880 885 890 895 900  
RKALESDFVSANLHHWIDLIFGYKQOGPAAVDAVNIHFPYFYGDMDLSSITDPLIKSTILGFVSNFGQVPKQLF  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRRR.RRRR.....RRRRRRR.....RRRR.....RRRR.....  
.....DDDDDD.....  
.....  
905 910 915 920 925 930 935 940 945 950 955 960 965 970 975  
TKPHPARTAAGKPLPGKDVSTFVSLFGHPQFFYSLSLRPSQVTVKDMYLFSLGSES PKGAIGHIVSTEXTILA  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....  
DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....  
.....  
980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050  
VERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAANGRCCLCAVCPSPTTIIVTSGTSTVVCVWELSM  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....  
DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
.....  
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125  
TKGRPRGLRLQALYGHTOAVTCLAASVTFSLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSGTI  
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RRRRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....  
DDD.....DDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
ddddd dddd  
.....  
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200  
VSCAGAHLSLWNVNQPLASITTANGPEGAITCCCLMEGPANDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG  
A.....AAA.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....  
RR.....RRRR.....RRRRRRR.....RRRRRRR.....RRRRRRR.....  
D.....DDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
.....  
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275  
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTS PAVTALAVSRMHTKLLVGDERGRIFCWSADG  
.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....  
DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....DDDDDDDDDDDD.....  
.....

FIG. 21  
Page 2 of 2



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ANALYSIS RESULTS OF THE PROGRAM TSITES.

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These are the results of the analysis of the file --> LY1484-2.TXT  
Beginning with residue: 1 and ending with residue: 647  
AMPHI Window size: 11

A - AMPHI mid points of blocks.  
R - Residues matching the Rothbard/Taylor motif.  
D - Residues matching the IAD motif.  
d - Residues matching the IED motif.

SEQ ID NO  
10,846

```

5  10  15  20  25  30  35  40  45  50  55  60  65  70  75
MLQKQKRDISNPEYLYLNTAAGRTCDYMOYVFPVFWLADYTSSETLNLANPKIFHDLSKPMGAQTKERKLKPI
...AAA...AAAAAAAAA...AAAAAAAAA...AAA
...RRRR...RRRRRRRR...RRRR...RRR
...ddd...

80  85  90  95 100 105 110 115 120 125 130 135 140 145 150
GRFKEVEKTEGDMTVQCHYTHYSSAIIVASYLVNMPPTQAPCALQGGSPDVADRMFHSVKSTWESASRENMSD
AAAAAAAAA...AAAAA...AAAAAAAAA...AA.AAAA..AA
R...RRRR.RRRR...RRRRRRRR...RRRRRRRR
...DDDDDDDDDD...

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
VRELTPFFYLPEPLTNCNGVEFOCMQDQTVLGDVQLPPNADGDPKPFISLHRKALESDFVSANLHHWIDLIFGY
AAAA...AAAAA...AAA...AAAAAAAAA
RRRR...RRRR...RRRR...RRRR.RRRR...RRRRRRRR
...

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQGGPAAVDAVNIFKPYFYGDRLSSITDPLIKSTILGFVSNFGQVPKQLPTKPHPARTAAGKPLPGKDVSTPV
AAAAAAAAA...AAAAA...AAAAAAAAA...AAAA
RRRR...RRRR...RRRR...RRRR...RRRR...DDDDDD...DDDDDD...DDDDDD
...

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPQPFYSLQSLRPSQVTVKDNLYFLSGSESPKGAIGHIVSTEKTLAVERNKVLLPPLMNRTPSNQFDDP
AAAAA...AAAAA...RRRRRRRR...RRRR
D...DDDDDD...

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYGSDKVLMTFENLAANGRCICAVCPSPITIVTSGTSTVVCVMEISMTKGRPRGLRLRQALYGHQAVTC
...AAAAAAAAA...
RRRR...DDDDDDDDDD...DDDDDD...DDDDDD...DDDDDDDDDD
...

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTFSLVSGSQDCTCILWDLHLTHVTLPAHREGISAITISDVSTIVSCAGAKLSLWVNGQPLASITT
...AAAAAAAAA...AAA...AAAAA...AAA
RRRRRRRR...RRRR...RRRR...DDDDDD...DDDDDD...DDDDDD
...

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ANGPEGAITCCCLNEGPAWDTSQIIITGSQDGMVRVWKTEDVIMSVPGRFAGEEPLAQPPSPRGHKEKNLALS
...AAAAA...RRRRRRRR...RRRR
D...DDDDDD...DDDDDD...

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSAPVTALAVSRNHTKLLVGDERGRIFCWSADG
...RRRR...
DDDDDDDD...DDDDDD...ddd

```

FIG. 22

# Ly1456P LifeSeqGold Clone Distribution

## Ly1456P LifeSeq Gold Search

LifeSeq Template	E Value of hit	Length (bp)	Libraries Found in		Clone Abundance		ORFs * (>50aa)	TMpred **
			Total #	Hemic & Immune #	Total Clone Count	Hemic & Immune		
238330_1	0	1442	55	21	78	33	294bp 177bp 252bp 198bp	No No No No

\* = Template sequence was searched for ORFs using MapDraw (4 potential ORFs identified).

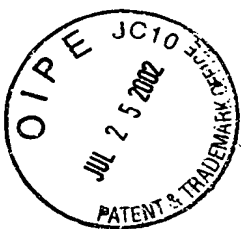
\*\* = Predicted ORFs were translated and were analyzed for potential TM regions using TMpred.

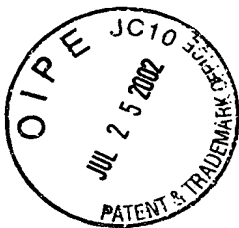
ORF#1 = 379>672 = 294bp = 98aa

ORF#2 = 555>734 = 177bp = 59aa

ORF#3 = 1037>1291 = 252bp = 84aa

ORF#4 = 1074>1274 = 198bp = 66aa

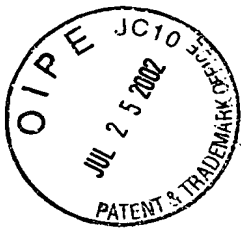




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SEQ ID NO: 10,475

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1 gcttctcccc tgggtcttca cgtgggtcccc gctgtctgtg cgttgtgtccc tgatctcttc
61 ttcttataag gaccccaatc atattggatt agagcccatc cacaggacct aaatttttcc
121 ctttaactctt tctctgtttg ccccaagaac actcaccagc agctctttgg gctgcagcgt
181 ttaccocaaaa gtaatttggg cacaacaacat cttcccttta ttattttcac ttgtcttag
241 tgtatcaact ttggaaaaca aagacatcat tctaogtata agacatcatt ctaggcttag
301 cgttctgtct ttagtagtgg catttccatt tagaataat tagaattctc gatcgtgtaa
361 aatgtcaaat ccgagaaaac atagcattcc tatgtgatca ttctcaaga gttgttggcc
421 aaagattcat ttgatatac ctatttttct gaaatagacg attctgatga ttgagatgat
481 ttgatgttta gttctgttta cacataactc caagaacagc ttttaaatte tactttcaca
541 ttgaaataca gtcagggttg tttatgtaaa attaaatgag ctctggccaa gcacgggtggc
601 tcatgccar aatcccagca ctttgggagg ctgagggtga cagatcactt gaggtcagga
661 gtttgacacc agcctgggca gcatggcgaa acccgtcttc tacaaaaaat acatatatat
721 tagccagatg tgggtgttga tgccgtgtgt cccagcttct cagggaagctg aggcaggaga
781 atcatttgaa cttgaggggc agagggttga gtgagccaa atgtgtccat ggaaccccaa
841 cctgggcaac agagcaagac tctgtctcaa aaaaaaaa aaatgtctgg agtgggctgc
901 acttttttct tctctaaaaa ggaataagggt taattatttc tttaaagaac cttagcaccaa
961 atacagtcac attcggagggt actgggggtt gggacttgaa catatgaatt ttgagggggc
1021 acaaggcatc ccattgacaca tgtgggaacc ggtataatct ctacagagac tagaatttag
1081 atttaacagc ttgaadacagc ttcaagttat tggtaacata caaaacaaaa acaattcaaa
1141 gccctttaca ttaaaattat tgaataaaaa ataactattt ctacaatgta taaaagggtat
1201 gctatgttta ttagctctac ttgtagctaa tctactttta tgtttcctta cagaaaaatc
1261 ttgacatttt atgtttccgt gtaagagatt gtacagaagg caaatttttg ttgtatgcaa
1321 taataatact ctaatacaaaa ttctgttatg aacttcatgt gcatatattt taatgtcat
1381 agcaattatt tttatgttgt attttcaaat aacttagatt tcatgcagca ttataaaact
1441 aactgggggt ggggacactg gctcatgctt gtaatctcaa cactttggga ggccaaaggc
1501 ggcagactgc ttaagccacg gagtttgaga ccatcctggg caacatggca aaacccctgc
1561 tctacaaaaa atacaaaaaa aacaaaaatt agccagacat ggtgtgtcac gctctgtctg
1621 ccagctactc aggaggttga cacaggagga tcaattgaac accggagggca gaggtctgcg
1681 tgagccagga ttgtgctact gcatctcagc tgggtgacac agccagagccc tgcctcaaaa
1741 caaaacaaaa caaaacaaaa acaaaacaga aaacagtgtg agaagtgttc attacccacc
1801 cccccccacc cccaaagctt tccaagctcc cgacccata cagaggcaca ggtgactgtg
1861 tgcaaaagtg cctgctgggc cccaaacgct cagtcacacc caccactgtc cttagctgac
1921 tcttgacccc tccaccttca atctagaccc cacacctatc ccaactatct ctcaagcaca
1981 gggggacatt gaataaagggt tttcttctctg tccctgcacc tccagacagc agagtgcatt
2041 ggtttcttag acagatcaga tctgtttaa acatttaaca aggtcaagat aacttaaaat
2101 agttaccaga caaaataga tggactagta catggacagc agctaacga gacatggggt
2161 gctacgttct tttatcacac atcagatctt gacatcatat tagtaagggt gtggggcggg
2221 gacatgccat gggcagggtg gggctgcagc tggccagact gagctggccc ttctgttag
2281 ttgaaccttg gggatgtgca gccgctgtgc aatgggtgcca cctgatgga ctttgtagaa
2341 taacctctct cctagttttt cttcatcttt aagttcctaa agagagactg aaatttcaaa
2401 tgggttctct tgttgcctat tattgtcaaa tgaaaagtgc aaactgttgg acccactct
2461 cttgattttt tttgtcttaa aaatgaaat ctcagctata ttcactgata tattatggaa
2521 agaacactgg acttaaggga tttgggttca gatccattt tgactctggag aatggaaata
2581 ggtatttgga aagtacttca acatctgcat gcccatttta tgactctggag aatggaaata
2641 ataggattct tgtgaggatt accaggaggt atatatgcac atctgcgtcc ataaactcaag
2701 cctgggtgtt gggagggtgt gcgtcaccat catgcatctt ctgaaggagg ctgaccagc
2761 tctaccttta atggctggga tttacttgtc ttttgggtcc ttccacctg ttgtccagca
2821 gaggctaaag tttgtgttga gggcatctct cagcagatga gttgagacca tctgtggcaa
2881 catggtcagg accaccttgg ggcctctgtg cagggcagtg cccacctga tgcctacgt
2941 ggtcagattg agagcataga catggggcca tgacctccat aaaccccccac ccagtgccac
3001 atggcagccc aaggaaacct cttagccctg ggttcttctg ctgtaaaacg aggttaacgt
3061 aacaagggga gctacttagt aaaccaaaaa aaaaaaaact aaactacaat tctgttctg
3121 ggtgtttttg ttttgttttg ttttggagtg ttatttggct gctgttttac tctattatcc
3181 cagagacaaa tgaagcgtaa gaggtgttct ttgcatfact ataaaggaa acttagact
3241 gggtaattta taagaaaaga gaagtctttt tgttttgggt ttgttttgag acagagtctt
3301 actcttattg cccaggctgg agtgcaatgg ttagatcttg actcactgca acctctgct
3361 cccagggttca agcaattctc ctgectcagc ctcttagta gctgggatta caggcatggg
3421 ccaccatgac cggctaattt cgtattttta gttagagacag agtttctcca tgttggctwg
3481 actggtctca aactcccaac ctcaagggtat ccgcttgcct tggcctccca aagtgtctgg
3541 attacgggca tgagccacag tgcctggcta gaaaaggagt ttaattggct cacagtcttc
3601 cagggtgtaa ggaagcatgg ccccaacatc tgcctcatct ctgaggaggc ctcaaggagc
3661 ttatgatcat ggcagaaagg gaagggggag caggcaogcc acatggcaca agcaggaaca
3721 agagagacag ctggtgttgg ggggtgccc agactcttca atgaccaggt ctcaagaa
3781 ttcactcact atgatcagga cagcaacca ccatgaggga tgggtccca tgatcccaac
3841 accctcccacc agatcccacc tccatcactg gggatcacaa tgcaacctga gatttgggag
3901 aggaacata tccaaactat atcaagcatc ttcttcccc ttctctctt cccctcctga
3961 tcttggggag aagaggctgc tgtgtgttct tgaagggtg agtgttctca cccaccccca
4021 acccccaag taagaaactc ttatgtttca gggcagggg gtgtggggag aggtgttccc
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4201 ggggggtgag catgaatacc cagaggctga gcttcaactc atcagcactg ctccggggga
4261 ccacagtgac tgaagagtg aactctgagc agtctcagg gogtctgag gcccgaggag
4321 ccagttctct gaattggtgca agacctgtc aggtccacag gaacccagaa gccaggaagc
4381 acaacaaatt ggatttccgc ccacgctgag tagatgggag ctagaaaaa aaagaaagcc
4441 aggtgtgttg gctcaogcct gtaatccag cacttgggga gggcggaggc gggcgtatcc
4501 ttgaagtcag gcatttgaga ccagcctggc caacatgggt ccaactact tgggtggctg
4561 atacaaaat tagctgggca tgggtggcat cacctgtaat cccactact tgggtggctg
4621 aggcagtaga atctctgaac ctgggaggca gagattgagc tgagctgaga ttgaccact
4681 gcactccagc ctgggcgaca gagtgagact ctgtcttaca aaaaaaaa aagaaaagag
4741 aaacaaagaa acaaaagaaa agaaaatcaa tggcccttgc gccagagtg ctggaggga
4801 gtccacactg acacgcccac ggggggagct gctgaaagca tccccagtc cagtgtgccc
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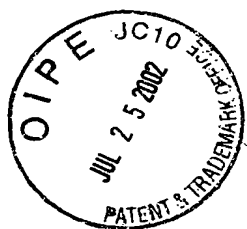


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4861 ccgtgagcac cgcacacctgt tccccgcttt cctggccacc gtacatacat ttgttcatgt  
4921 ttatagactc tgaatataga gacccacacac aagaagagaa aggttcagaa aaacaatgtt  
4981 atgacctgct tcctgaggca ccttgccctgc aggaagtgtt ttccacagca agaaattctg  
5041 actccaggac ccatattttt agcaggaaca tggtcagtca acacacatcc tctaggcctg  
5101 cctcggacca gatgaccagg aggaagcagc cgtgagtcac agggagaaag ccggtggttc  
5161 tgacagggac gcctgctgct ccgcccggga acagctttcc cctggtttca gtttagaaag  
5221 tcaggggacg cctgaccaca caaggctcac gggaaactgt gaggcgccgc cctcaggcca  
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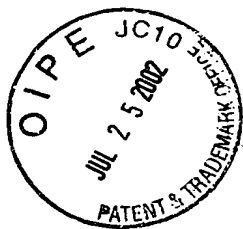




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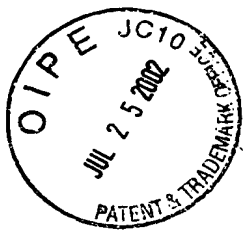
FIG. 24  
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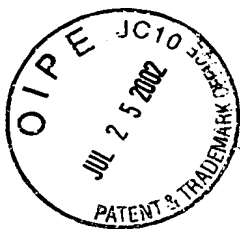
FIG. 24



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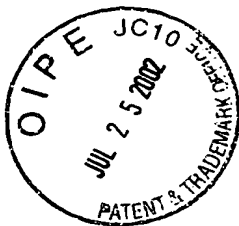
FIG. 24



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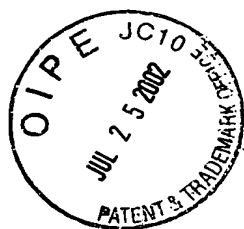
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FIG. 24



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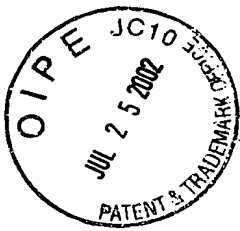
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FIG. 24

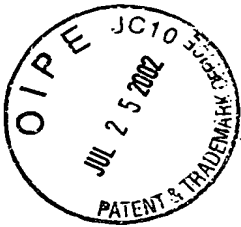


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FIG. 24  
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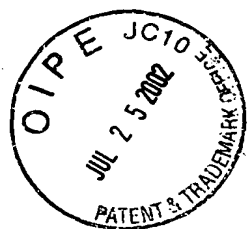




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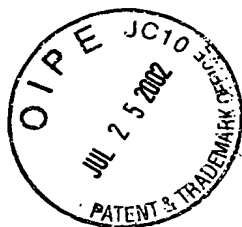
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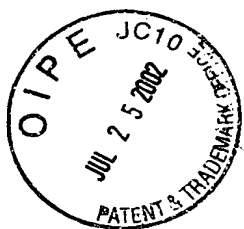
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SER ID NO: 10,476

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FIG. 25

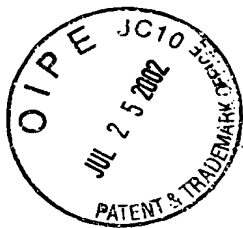


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FIG. 26



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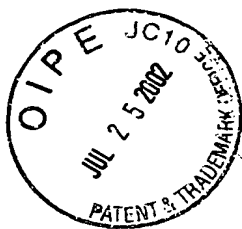
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## Lyl488 DNA Sequence (mRNA) (SERID NO: 10,970)

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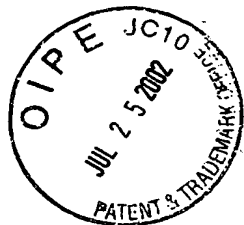
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## TMpred Report for Ly1488 (SEQUENCE: 10,969)

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Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1488Rp3-329A5Chr6 has 756 amino acids and 1 Transmembrane Domains  
Transmembrane Domain 1: 199 - 220 Score: 1.3061

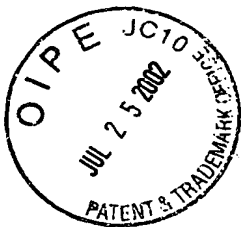


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Lyl449 and Lyl480 matches Lung cancer associated  
polynucleotide sequence SEQ ID 10,476

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FIG. 29

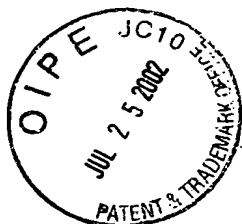


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Homo sapiens chromosome 17, clone RP11-956N15, complete sequence (bp1-10 000)

(SEQ ID NO: 10,474)

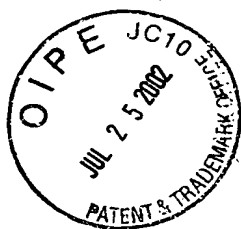
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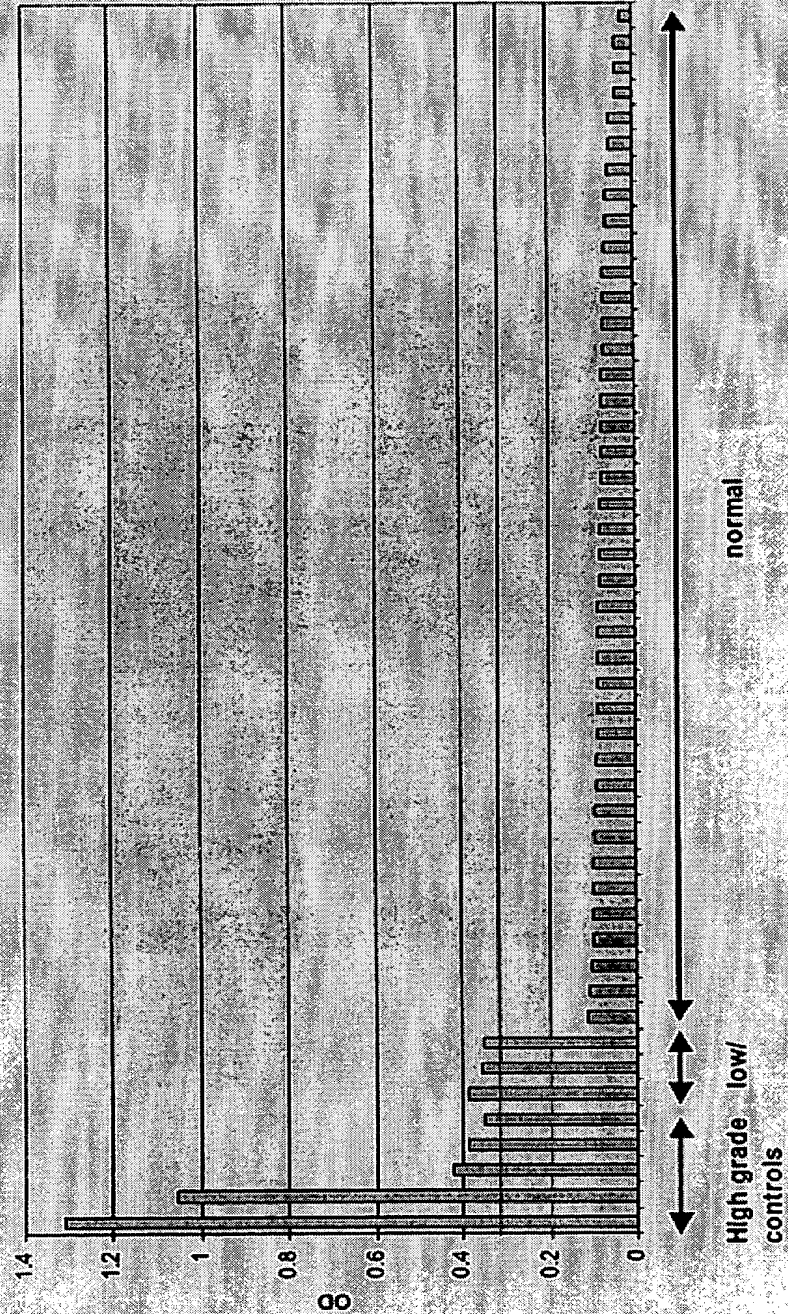




50/52

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**Detection of Ly 148P specific serum antibodies in  
lymphoma patients**



**FIG. 31**



# Detection of TCL-1 specific serum antibodies in lymphoma patients

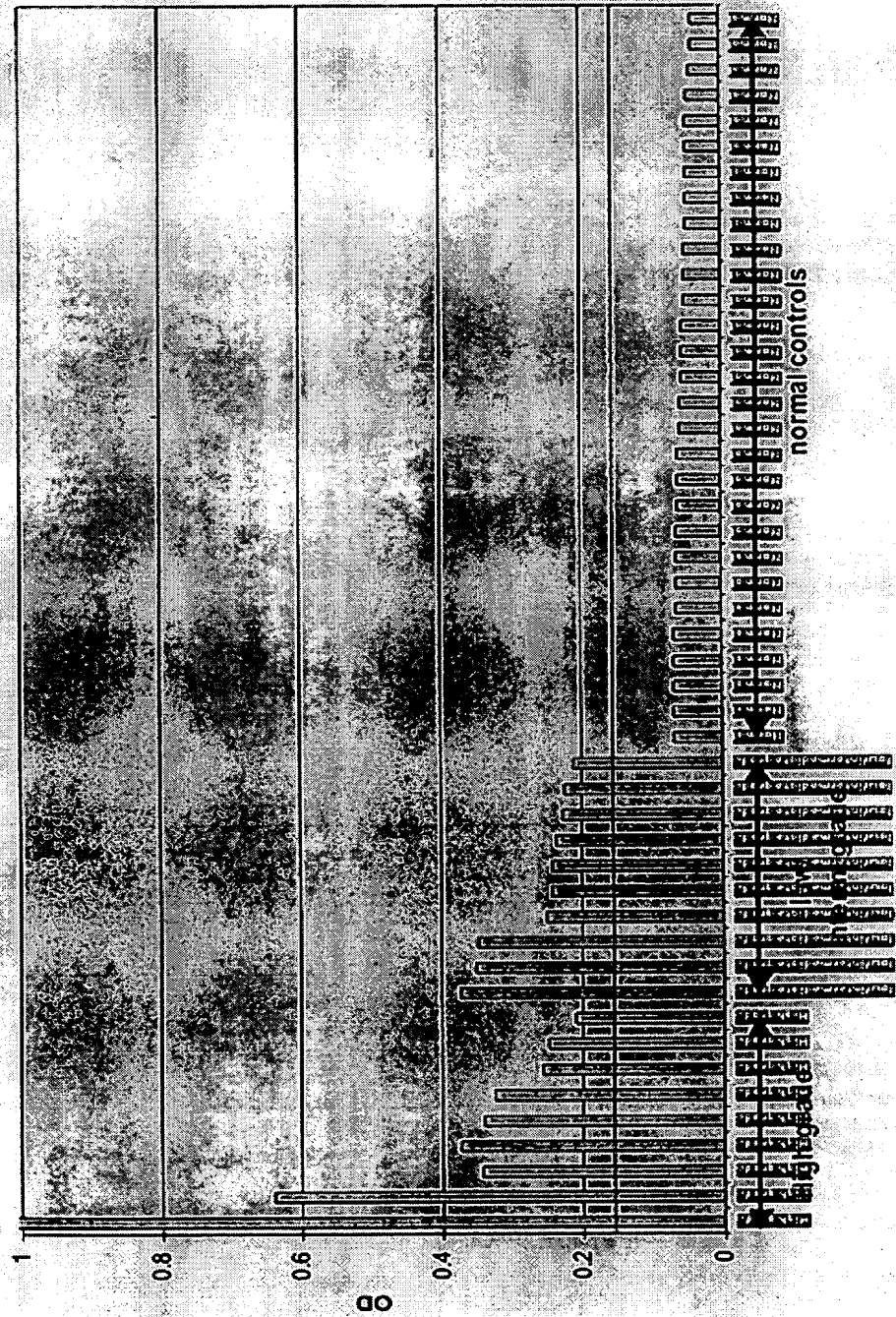


FIG. 32